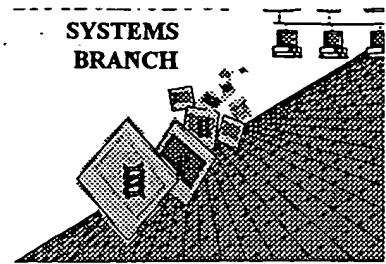


RAW SEQUENCE LISTING **ERROR REPORT**



#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/445,375

Art Unit / Team No. : 1632

Date Processed by STIC: 5/18/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/445,375

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 **Misaligned Amino Acid
Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 **Use of <213>Organism
(NEW RULES)** Sequence(s) are missing this mandatory field or its response.
- 12 **Use of <220>Feature
(NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1632

RAW SEQUENCE LISTING

DATE: 05/18/2000

PATENT APPLICATION: US/09/445,375

TIME: 12:23:30

Input Set : A:\DU23SEQ.txt

Output Set: N:\CRF3\05182000\I445375.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Kingsman, Susan M
4 Bebbington, C.
5 Ellard, F.
6 Carroll, Miles
8 <120> TITLE OF INVENTION: VECTOR
10 <130> FILE REFERENCE: DY0U23.001APC
12 <140> CURRENT APPLICATION NUMBER: US/09/445,375
13 <141> CURRENT FILING DATE: 1999-12-02
15 <160> NUMBER OF SEQ ID NOS: 24
17 <170> SOFTWARE: PatentIn Ver. 2.0
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25 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA
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34 rstdsavyy carstatgat tacgaactat gttatggact actgggggtca agtaacctca 420
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39 cagtctccta cactgctcat atvawykgt cctatacatc cagtcgctac gctggagtcc 720
40 ctgatcgctt cattggcagt sytssryagv drgsggatat gggacggatt tcactttcac 780
41 catcagcact ttgcaggctg aagagygttdt tstadcctgg cagtttattt ctgtcagcaa 840
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56 dggtgaagcc tggggcttca gtgaagatat cctgcaagcc ttctggttac tvkgasvksc 180
57 kasgycattc actggctact acatgcactg ggtgaagcag agccatggaa agagcstggy 240
58 mhwvkshgks cttgagtggg ttggacgtat taatcctaac aatggtgtta ctctotacaa 300
59 wgrnnngvty nccagaaatt caaggacaag gccatattaa ctgtagacaa gtcattccacc 360
60 akkdkatvdK sstcagccta catggagctc cgcagcctga catctgagga ctctgcggtc 420

give source of genetic material -
see circled portion
of item 12
on Eva summary
sheet

see
item 10
on Eva
summary
sheet

item 10
W-->

RAW SEQUENCE LISTING DATE: 05/18/2000
 PATENT APPLICATION: US/09/445,375 TIME: 12:23:30

Input Set : A:\DU23SEQ.txt
 Output Set : N:\CRF3\05182000\I445375.raw

item 10 for all labeled lines

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68 tgggacggat ttactttca ccatcagdrq sgvgtdttsc actttgcagg ctgaagacct 900
69 ggcagtttat ttctgtcagc aagattatat adavyodyat tctctccga cgttcgggtg 960
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72 ctgggctgcc tggtaagga ctacttcccc gsggtaagcv kdyaaccggt gacgggtgctg 1140
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79 cggaccctgt aggtcacatg cgtggtggtg gacgtgagcc acmsrtvte vdvshgaag 1560
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84 aaktcatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc ctgcskakgr 1860
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W--> 89 tvdkswrcag ggaacgtct tctcatgtc cgtgatgcat gaggtctgc acaaccagnv 2160
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104 sgtgttatcc acgtgaccaa ggaagtgaag gaagtggcaa cgtgtctctg tgvhvtkvkv 180
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106 atrywaaagg agaagaaat ggtgctgact atgatgtctg gggacatgaa tatatkkmv 300
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109 arsdgtycvt gttctgaagt atgaaaaaga cgctttcaag cgggaacacc tggctgaagv 480
110 kykdakrhat gacgttatca gtcaagctg acttccctac acctagtata tctgactttv 540
111 tsvkadtsd gaaattccaa ctctaatat tagaaggata atttgctcaa cctctggagg 600
W--> 112 tsnrrestsg gttttccaga gcctcacctc tctggttg gaaatggaga agaattaaat 660

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item 10

RAW SEQUENCE LISTING DATE: 05/18/2000
 PATENT APPLICATION: US/09/445,375 TIME: 12:23:30

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 Output Set: N:\CRF3\05182000\I445375.raw

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 117 ctttkhdggg gsvcagcagt ctggacctga cctggtgaag cctggggcct cagtgaagat 960
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 W--> 120 aatcctaack shgkswgrnn aatgggtgta ctctctacaa ccagaaattc aaggacaagg 1140
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 124 tcagtcaccg tctcctcagg yvmdywgvtv vtvsstggtt ggtggggagc gtgggtggcg 1380
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 126 attcctgctt gtcttcagcag gagacagggg tvmtttvsag drvaccataa cctgcaaggc 1500
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 129 gtccctgacg gcttcatctg cagtggatat gggacgsrya gydrsgsygt gatttcactt 1680
 130 tcaccatcag cacttttcag gctgaagacc tggcagttta dttstadavy tttctgtcag 1740
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 W--> 145 caatttgcaa actctcaaaa ccaaagcctg agtgagctag tagtatttca nsnssvtggt 180
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 152 tgctcatcta tacacgggta cccagaacct aagaagatga gtgttttgc csshgykkms 600
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 W--> 155 sssvsttccc tgatgttacg agcaatatga ccatcttctg tattctggaa actgadvtstn 780
 156 mtctdcaaga cgcggctttt atcttcacct ttctctatag agcttgagga ccctcktrss 840
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/445,375
 DATE: 05/18/2000
 TIME: 12:23:30

Input Set : A:\DU23SEQ.txt
 Output Set: N:\CRF3\05182000\I445375.raw

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170 caactgtcca agtcagtgaa agataaggta ttgctgcctt gccgttacaa ctctccgcat 180
171 gaagatgagt ctgaagaccg aatctactgg caaaaacatg acaaagtggg gctgtctgtc 240
172 attgtctgga aactaaaagt gtggcccag tataagaacc ggactttata tgacaacact 300
173 acctactctc ttatcatcct gggcctgggc ctttcagacc ggggcacata cagctgtgtc 360
174 gttcaaaaga aggaaagagg aacgtatgaa gttaaactct tggctttagt aaagtgtgtc 420
175 atcaaagctg acttctctac ccccaacata actgagctcg gaaaccatc tcgagacact 480
176 aaaaggatta cctgctttgc ttccgggggt ttcccaaagc ctgccttctc ttggttgga 540
177 aatggaagag aattacctgg catcaatcag acaatttccc aggatcctga atctgaattg 600
178 tacaccatta gtacccaact agatttcaat acgactcgca accacaccat taagtgtctc 660
179 attaaatatg gagatgctca cgtgtcagag gacttcacct gggaaaaacc ccagaagac 720
180 cctcttgata gcaagcccgg ggtggtggg agcggtggg gcggcagtg cgcgcgga 780
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201 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA
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207 agcagagcca tggaaaagag cttgagtgga ttggacgtat taatcctaac aatggtgtta 240
208 ctctctacaa ccagaaattc aaggacaagg ccatattaac tgtagacaag tcatccacca 300
209 cagcctacat ggagctccgc agcctgacat ctgaggactc tgcggtctat tactgtgcaa 360
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/445,375
 DATE: 05/18/2000
 TIME: 12:23:30

Input Set : A:\DU23SEQ.txt
 Output Set : N:\CRF3\05182000\I445375.raw

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233 ccaagaccag cggcccgctg gctgcccgg aagtctatgc gtttgcgacg ccgagtggtg 1800
234 cggggagcgg ggacaagcgc accctgcctt gcctgatcca gaacttcacg cctgaggaca 1860
235 tctcgggtga gtggctgcac aacgaggtgc agtcccgga cgcccggcac agcacgacgc 1920
236 agcccgcaa gaccaaaggg tccggcttct tctcttcag ccgctggag gtgaccaggg 1980
237 ccgaatggga gcagaagat gatgtcatct gccgtgcagt ccatgaggca gcgagccct 2040
238 cacagaccgt ccagcgagcg gtgtctgtaa atcccggtaa atgagagctc 2090

```

240 <210> SEQ ID NO: 7
 241 <211> LENGTH: 945
 242 <212> TYPE: DNA
 243 <213> ORGANISM: Artificial Sequence
 245 <220> FEATURE:
 246 <223> OTHER INFORMATION: Description of Artificial Sequence DNA
 248 <400> SEQUENCE: 7

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249 atggcttgca attgtcagtt gatgcaggat acaccactcc tcaagtttcc atgtccaagg 60
250 ctcattcttc tctttgtgct gctgattcgt ctttcacaag tgtcttcaga tgttgatgaa 120
251 caactgtcca agtcagttaa agataaggta ttgtgcctt gccgttacia ctctccgcat 180
252 gaagatgagt ctgaagaccg aatctactgg caaaaacatg acaaagtggg gctgtctgtc 240
253 attgctggga aactaaaagt gtggcccag tataagaacc ggactttata tgacaacact 300
254 acctactctc ttatcatcct gggcctgggt ctttcagacc ggggcacata cagctgtgtc 360
255 gttcaaaaaga aggaagagg aacgtatgaa gttaaacact tggctttagt aaagtgtgct 420
256 atcaagctg acttctctac cccaacata actgagtcgt gaaacccatc tgcagacact 480
257 aaaaggatta cctgctttgc ttccgggggt ttccaaaagc ctgccttctc ttggttgtaa 540
258 aatggaagag aattacctgg catcaatacg acaatttccc aggatcctga atctgaattg 600
259 tacaccatta gtaccgaact agatttcaat acgactcgca accacacat taagtgtctc 660
260 attaaatatg gagatgctca cgtgtcagag gacttcacct gggaaaaacc cccagaagac 720
261 cctcctgata gcaagcccgg ggggtgtggg agcgggtggg gcggcagtg gcggcgcgga 780
262 actagtaata gtgactctga atgtcccctg tcccacgatg ggtactgct ccatgatggt 840
263 gtgtgcatgt atattgaagc attggacaag tatgcatgca actgtgtgtg tggctacatc 900
264 ggggagcgat gtcagtaccg agacctgaag tgggtgggaa tgcgc 945

```

266 <210> SEQ ID NO: 8
 267 <211> LENGTH: 47
 268 <212> TYPE: DNA
 269 <213> ORGANISM: Artificial Sequence
 271 <220> FEATURE:
 272 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 273 OLIGONUCLEOTIDE

VERIFICATION SUMMARY DATE: 05/18/2000
PATENT APPLICATION: US/09/445,375 TIME: 12:23:31

Input Set : A:\DU23SEQ.txt
Output Set: N:\CRF3\05182000\I445375.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:31 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:31 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:35 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:35 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:42 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:42 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:59 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:59 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:62 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:62 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:66 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:66 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:70 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:70 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:73 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:76 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:76 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:103 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:103 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3

VERIFICATION SUMMARY DATE: 05/18/2000
PATENT APPLICATION: US/09/445,375 TIME: 12:23:31

Input Set : A:\DU23SEQ.txt
Output Set: N:\CRF3\05182000\I445375.raw

L:103 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:105 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:105 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:108 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:108 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:112 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:143 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24